



A:Molecule type: DNA  
A:Residues: 1-1957 <CON>  
A:Cross-references: EMBL:270690; PIDN:CAA94624.1; GSPDB:GN00066; SPDB:SPAC1F3.06C  
A:Experimental source: strain 972h; cosmid c1f3  
A:Gene: SPDB:SPAC1F3.06C  
A:Map position: 1

Query Match 16.0%; Score 170.5; DB 2; Length 1957;  
Best Local Similarity 23.6%; Pred. No. 0.048; Mismatches 92; Indels 43; Gaps 6;  
Matches 58; Conservative 53;

Oy 15 EENVLDREFLNKELNDVNRALQSQDKERKSDVITDITLDTLEENATVATVSLQALGKAE 74  
Db 1386 EDNOLATNKLKQNDHLNQLRKLKEDVLEKESLIISLESISLNRQKSSSLDKKNELE 1445  
Oy 75 -MLCSTLKKOMKYLEQOODETKOAOEAGRLRSKKMTM-----EQIELL--LQSLP 123  
Db 1446 HMLDTSRKNSSLMERIESINSLDDKSFELASAVEKLGALOKLHSESLSLMENIKSOLQ 1505  
Oy 124 EVEEMIRDMGVGQSAVEOLAVYCVSLKKYEN-----LKEARK 161  
Db 1506 EAKKTIQ--VDESTIOELDEHTTASKNYEGSKLNDKDSIIDLSEBNIEQLNNLLAEKKS 1562  
Oy 162 ASGEVADKLRLKDLFSSRSKL-----QTVVSELDQAKLELSAOKDLQSDAKREIMSLKK 214  
Db 1563 AVKRLSTEKESIELQFNLSRLADLEYHKSQVESELSRSKRLKSLTEBELQALNENLSLTT 1622  
Oy 215 KLTMLQ 220  
Db 1623 RMLDLQ 1628

RESULT 3  
A26655  
myosin heavy chain [similarity] - slime mold (Dictyostellium discoideum)  
N:Contains: myosin ATPase (EC 3.6.1.32)  
C:Species: Dictyostellium discoideum  
C:Date: 05-Oct-1988 #sequence\_revision 05-Oct-1988 #text\_change 02-Feb-2001  
C:Accession: A26655; A24728; S00250  
R:Warrick, H.M.; De Lozanne, A.; Leinwand, L.A.; Spudich, J.A.  
Proc. Natl. Acad. Sci. U.S.A. 83, 9433-9437, 1986  
A:Title: Conserved protein domains in a myosin heavy chain gene from Dictyostellium disc  
A:Reference number: A26655; MUID:87092266  
A:Accession: A26655  
A:Molecule type: DNA  
A:Residues: 1-2116 <MAR>  
A:Cross-references: GB:M14628; GB:M11938; NID:g167834; PIDN:AAA33227.1; PID:g167835  
R:DeLozanne, A.; Lewis, M.; Spudich, J.A.; Leinwand, L.A.  
Proc. Natl. Acad. Sci. U.S.A. 82, 6807-6810, 1985  
A:Reference number: A24728; MUID:86016788  
A:Accession: A24728  
A:Molecule type: mRNA  
A:Residues: 2035-2116 <DEL>  
R:Wagle, G.; Noegel, A.; Scheel, J.; Gerisch, G.  
FEBS Lett. 227, 71-75, 1988  
A:Title: Phosphorylation of threonine residues on cloned fragments of the Dictyostellium  
A:Reference number: S00250; MUID:88112226  
A:Accession: S00250  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1734-1893 <RAG>  
C:Comment: The rod domain is highly periodic, containing a pattern of 7-residue repeats  
C:Superfamily: myosin heavy chain; myosin motor domain homology  
C:Keywords: actin binding; ATP; coiled coil; hydrolase; nucleotide binding; P-loop; phos  
F:81-818/Domain: globular head <HED>  
F:89-747/Domain: myosin motor domain homology <MMOT>  
F:179-186/Region: nucleotide-binding motif A (P-loop)  
F:819-2116/Domain: alpha-helical rod <ROD>

Query Match 15.4%; Score 164.5; DB 2; Length 2116;

Best Local Similarity 25.4%; Pred. No. 0.11;  
Matches 68; Conservative 56; Mismatches 87; Indels 57; Gaps 11;

Oy 5 NKLFFDLAQLQEEENVLD-REFLNKELNDVNRALQSQDKERKSDVITDITLDTLEENATVATVSLQALGKAE 60  
Db 852 DKLKSLKDTESNVIDLQROLKAEKETLAMYDSKDALQALQRELEIWEDESELDK 911  
Oy 61 ATTVSLQ-----QALGKAEMLCSTLKKOMKYLEQOODETKOAOEAGRLRS 106  
Db 912 LALENLQNRKSVREKVDLEELQEBOKLRNTLEKLKKYEELEBKRVNDGSDPTIS 971  
Oy 107 KKKTMEQIELLLQSLPEVEEMI---RDMGV-----GQSAVBOLAVCVS----- 148  
Db 972 R---LEKIKDELQKEVEELTESFSESKDKGVLEKTRVRLQSELDDLTVRLDSEFTKDKSE 1028  
Oy 149 ---LKKREYNKLEARKA-SGEVADKLRLKDLFSSRSKTIQTVSELDQ-----AKLELK 196  
Db 1029 LTRQKKLEELQYQVLAETAKLAQE--AANKRLOGEYTELNERFNSSEVTARSNVE 1086  
Oy 197 SAOKDLQS---ADKEIMSLKKLTMLQ 220  
Db 1087 KSKLTESOLAVANNLEDEKKNRDALE 1114

RESULT 4  
JH0720  
tanablin - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 21-Jul-2000  
C:Accession: JH0720  
R:Hemmati-Brivanlou, A.; Mann, R.W.; Harland, R.M.  
Neuron 9, 417-428, 1992  
A:Title: A protein expressed in the growth cones of embryonic vertebrate neurons defi  
A:Reference number: JH0720; MUID:92398961  
A:Accession: JH0720  
A:Molecule type: mRNA  
A:Residues: 1-1744 <HEM>  
A:Cross-references: GB:M9387; NID:g214816; PIDN:AAA49966.1; PID:g214817  
A:Experimental source: tadpole head  
C:Keywords: intermediate filament

Query Match 15.3%; Score 163.5; DB 2; Length 1744;  
Best Local Similarity 25.8%; Pred. No. 0.1;  
Matches 60; Conservative 61; Mismatches 73; Indels 39; Gaps 9;

Oy 12 AOEENVLDREFLNKELNDVNRALQSQDKERKSDVITDITLDTLEENATVATVSLQALG 71  
Db 33 ALREEN---ELLKREIHSLSRSKSEKRCMKKNHEEM-KLRDALDDGHNREY----- 80  
Oy 72 KAEMLCSTLKKOMKYLEQOODETKOAOEAGRLRSKKMTMEQIELLLQSO-----P 123  
Db 81 QAEWVRDSIYEIEFVKRCLEBKQAKEDAKKESESKLLBEETRAOIMLKERIGOLEA 140  
Oy 124 EVEEMIRDMGVGQSAVEOLAVYCVSLKREYNLEKARKA--SGEVADKLRL--DLFSS-- 177  
Db 141 ELEDILRHEEKALME---ELASFQRLNFPRAVPAFVPEVDVARRLSEIMQGA 197  
Oy 178 ---NSKLTQVSELDQAKLELSAOKD-----LQSDAKREIMSLKKLTMLQ 220  
Db 198 EYKSEVSVLEAGLSESKENLRKVLSENNKONRLLQSDIKDELVSLSKMKKALE 250

RESULT 5  
T42722  
male-enhanced antigen-2 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 11-Jan-2000  
C:Accession: T42722  
R:Kondo, M.; Sutoh, S.  
DNA Seq. 7, 71-82, 1997  
A:Title: Cloning and molecular characterization of cDNA encoding a mouse male-enhance  
A:Reference number: 222242; MUID:97217683



F:91-780/Domain: myosin motor domain homology <MMO>

Query Match 15.0%: Score 159.5; DB 2; Length 2139;  
Best Local Similarity 24.0%: Pred. No. 0.21;  
Matches 60; Conservative 49; Mismatches 96; Indels 45; Gaps 7;

QY 5 NKLFDL--AOEENVLNREFLNELDVNRQLSQKDEKRDSDVI-----ID 50  
DB 1144 NKIBEDLNNAQRKIKLEDEDEITKGA--DV-SQYLQKQKEVESQJLAKKQEEKEATGNVYK 1200  
QY 51 TLRDITLEERNATVVSLOQALGKAEMLCSTLKKOMKYLEQOODETKQAOEEAGRLSKMKT 110  
DB 1201 NKEKIKKEKELEIOSLOEKLEDETEVEKEDAEKKKEIEK---EMKALQEEKENVESKNS 1257  
QY 111 MEQITELLQSQLPVEEEMIRDMGVQGSVAVEQLAVYCVSLKEVEYELKPKARKASGVAAKL 170  
DB 1258 TEKDKKKLEDDNLDKDTQADMTADNEKLKAKADEQLNEVDNHNHKAADADELNRK 1317  
QY 171 R----KDLFSSRSKLQ-----TVSELDQAKLELKSACQKDLQSA 205  
DB 1318 KAQSKKELNSLKAELFALTAKKSVESKNKDSSENKALSEIDQANKELKNIGADLTKA 1377  
QY 206 DKEIMSLKKK 215  
DB 1378 TADLQEANEK 1387

RESULT 9  
S67593  
Transport protein USO1 - yeast (Saccharomyces cerevisiae)  
N:Alternate names: protein D2552; protein YDL058w  
C:Species: Saccharomyces cerevisiae  
C:Date: 12-Jul-1996 #sequence.revision 12-Jul-1996 #text.change 21-Jul-2000  
C:Accession: S67593; A38455; S30782  
R:Bioceker, H.; Brandt, P.  
Submitted to the Protein Sequence Database, July 1996  
A:Reference number: S67593  
A:Accession: S67593  
A:Molecule type: DNA  
A:Residues: 1-1790 <BLO>  
A:Cross-references: EMBL:Z74106; NID:91431056; PID:e253003; PID:91431059; MIPS:YDL058w  
A:Experimental source: strain S288c  
R:Nakajima, H.; Hirata, A.; Ogawa, Y.; Yonehara, T.; Yoda, K.; Yamasaki, M.  
J. Cell Biol. 113, 245-260, 1991  
A:Title: A cytoskeleton-related gene, USO1, is required for intracellular protein transp  
A:Reference number: A38455; MUID:91185402  
A:Accession: A38455  
A:Molecule type: DNA  
A:Residues: 1-389, 'TA', '392-724', 'S', '726-1790 <NAK>  
A:Cross-references: GB:X54378; NID:94777; PIDN:CAA38253.1; PID:94778  
A:Note: the authors translated the codon ACT for residue 768 as Ile  
R:Hosteier, M.K.; Herman, D.J.; Bendel, C.M.; McClellan, M.; Tao, N.; Kendrick, K.E.  
submitted to the EMBL Data Library, February 1993  
A:Description: An integrin analogue in Saccharomyces cerevisiae.  
A:Reference number: S30782  
A:Accession: S30782  
A:Molecule type: DNA  
A:Residues: 71-846, 'E', '848-923', 'K', '925-1252', 'I', '1254-1318', 'V', '1320-1460', 'S', '1462-1580', 'S  
A:Cross-references: EMBL:L03188  
C:Genetics:  
A:Gene: SGD:USO1; INT1  
A:Cross-references: SGD:S0002216; MIPS:YDL058w  
A:Map position: 4L  
C:Keywords: coiled coil; transmembrane protein  
F:326-342/Domain: transmembrane #status predicted <TM1>  
F:394-410/Domain: transmembrane #status predicted <TM2>  
F:617-633/Domain: transmembrane #status predicted <TM3>

Query Match 14.9%: Score 159; DB 2; Length 1790;  
Best Local Similarity 23.7%: Pred. No. 0.19;  
Matches 61; Conservative 57; Mismatches 85; Indels 54; Gaps 9;

QY 1 RTIINKLFFDLAQ---EEENVLDREFLK-----NELDNVRAQLSQKDEKRDSDVI 48  
DB 1369 RKLNEGSSITTOEYSEKINFLDEELIRLQENENELKAKEDINTSEL-EKSLSND----- 1423  
QY 49 IDTLRDITLEERNATVVSLOQAL-----GKAEMLCSTLKKOMKYLEQOODETKQAOEE 100  
DB 1424 -----ELLEEKQNTIKSLQDELITSLYKDKITRNDEKLSTIERDNKRDLSELTKEQLRAQES 1478  
QY 101 AGRLRSKKTKMEQITELLQSQLPVEEEMIRDMGVQGSVAVE---QLAVYCVSLKKEVENL 156  
DB 1479 KAKVEEGKLKLEESSSKKAELEKSKEMMKRL---ESTIESNETLSSMETIKRSDEKL 1535  
QY 157 KEARKASGEVADKLR-----KDLFSSRSKLQTVY---SELDQAKLELKSQ 199  
DB 1536 ESKKSAEEDIKNLQHEKSDLSIRNESKDIIEELKSLRLIANSGSLELTQKQLNNAQ 1595  
QY 200 KDLSQADKEIMSLKKKL 216  
DB 1596 EKIRINAEENTVLKSKL 1612

RESULT 10  
S06006  
myosin beta heavy chain, cardiac muscle [similarity] - rat  
N:Contains: myosin ATPase (EC 3.6.1.32)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 31-Dec-1993 #sequence.revision 31-Dec-1993 #text.change 19-Jan-2001  
C:Accession: S06006; S07536; I67441; A02989  
R:Kraft, R.; Bravo-Zehnder, M.; Taylor, D.A.; Leinwand, L.A.  
Nucleic Acids Res. 17, 7529-7530, 1989  
A:Title: Complete nucleotide sequence of full length cDNA for rat beta cardiac myosin  
A:Reference number: S06006; MUID:90016823  
A:Accession: S06006  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-1935 <RA>  
A:Cross-references: EMBL:X15939; NID:956656; PIDN:CAA34065.1; PID:956657  
R:McNally, E.M.; Kraft, R.; Bravo-Zehnder, M.; Taylor, D.A.; Leinwand, L.A.  
J. Mol. Biol. 210, 665-671, 1989  
A:Title: Full-length rat alpha and beta cardiac myosin heavy chain sequences. Compari  
A:Reference number: S07535; MUID:90139919  
A:Accession: S07536  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-950, 'RK', '953-1935 <MCN>  
R:Mahdavi, V.; Lompre, A.M.; Chambers, A.P.; Nadal-Ginard, B.  
Eur. Heart J. 5, 181-191, 1984  
A:Title: Cardiac myosin heavy chain isozymic transitions during development and under  
A:Reference number: I53305; MUID:85179510  
A:Accession: I67441  
A>Status: translated from GB/EMBL/DBD  
A:Molecule type: mRNA  
A:Residues: 1871-1935 <RES>  
A:Cross-references: GB:M32698; NID:920598; PIDN:AAA41659.1; PID:920599  
R:Mahdavi, V.; Periasamy, M.; Nadal-Ginard, B.  
Nature 297, 659-664, 1982  
A:Title: Molecular characterization of two myosin heavy chain genes expressed in the  
A:Reference number: A02988; MUID:82220036  
A:Accession: A02989  
A:Molecule type: mRNA  
A:Residues: 1524-1528, 'V', '1530', 'R', '1532-1730', 'H', '1732-1783', 'K', '1785-1850', 'N', '1852-185  
A:Cross-references: GB:J00752; NID:9205577; PIDN:AAA41654.1; PID:9205578  
C:Superfamily: myosin heavy chain; myosin motor domain homology  
C:Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; hydrolase; methyl  
F:178-185/Domain: myosin motor domain homology <MMOT>  
F:178-185/Region: nucleotide-binding motif A (P-loop)  
F:548-585/Region: actin binding #status predicted  
F:655-677/Region: actin binding #status predicted  
F:839-1935/Domain: actin binding #status predicted  
F:839-1279/Region: coiled coil #status predicted <COI>  
F:1280-1935/Region: light meromyosin  
F:129/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted





```
OY   178 RSKLQT---VSELDQAKLEKSAQKDLSADKEIMSLKKLTMLQ    220  
      |:| :|          |::|| :| ||:|| ::| :| :|  
Db   1375 RTKYETDAIORTTEELFEAAKKL--AQR-LQDAEEHVEAVNAKCASTE    1418
```

## RESULT 17

myosin heavy chain, skeletal muscle, embryonic - rat  
 N:Contains: myosin ATPase (EC 3.6.1.32)  
 C:Species: Rattus norvegicus (Norway Rat)  
 C:Date: 31-Dec-1993 #sequence,revision 31-Dec-1993 #text,change 19-Jan-2001  
 C:Accession: A24922; #status predicted  
 R:Strehler, E.E.; Strehler-Page, M.A.; Perliard, J.C.; Periasamy, M.; Nadal-Ginard, B.  
 J. Mol. Biol. 190, 291-317, 1986  
 A:Title: Complete nucleotide and encoded amino acid sequence of a mammalian myosin heavy  
 A:Reference number: A24922; MUID:87060988  
 A:Accession: A24922  
 A:Molecule type: DNA  
 A:Residues: 1-1940 <STR>  
 A:Molecule type: DNA  
 A:Cross-references: GB:X04267; GB:X05004; NID:g56658; PIDN:CAA27817.1; PID:g1619328  
 R:Strehler, E.E.; Mandavil, V.; Periasamy, M.; Nadal-Ginard, B.  
 J. Biol. Chem. 260, 468-471, 1985  
 A:Title: Intron positions are conserved in the 5' end region of myosin heavy-chain genes  
 A:Reference number: A22538; MUID:85080119  
 A:Accession: A22538  
 A:Molecule type: DNA  
 A:Residues: 1-168 <STR>  
 A:Cross-references: GB:U00370; GB:M10135; NID:g205580; PIDN:AAA1655.1; PID:g554476  
 R:Periasamy, M.; Wydosy, R.M.; Strehler-Page, M.A.; Strehler, E.E.; Nadal-Ginard, B.  
 J. Biol. Chem. 260, 15856-15862, 1985  
 A:Title: Characterization of cDNA and genomic sequences corresponding to an embryonic my  
 A:Reference number: A24263; MUID:6605474  
 A:Accession: B24263  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1358-1490, 'G' <PER>  
 A:Cross-references: GB:K03468; NID:g205573; PIDN:AAA1652.1; PID:g205574  
 A:Experimental source: clone pMHC-72  
 C:Genetics:  
 A:Introns: 68/3; 116/3; 169/1  
 A:Note: the list of intron positions may be incomplete  
 C:Superfamily: myosin heavy chain; myosin motor domain  
 C:Keywords: actin binding; ATP: coiled coil; hydrophase; methylated amino acid; muscle co  
 F:179-186/Domain: myosin motor domain homology <MMOT>  
 F:89-757/Domain: nucleotide-binding motif A (P-loop)  
 F:179-186/Region: nucleotide-binding motif A (P-loop)  
 F:349-586/Region: actin binding #status predicted  
 F:656-678/Region: actin binding #status predicted  
 F:840-1940/Domain: coiled coil #status predicted <COI>  
 F:840-1280/Region: S2  
 F:1281-1940/Region: light meromyosin  
 F:130/Modified site: N6,N6,N6-L-Trimethyllysine (lys) #status predicted  
 F:185/Binding site: ATP (lys) #status predicted  
 F:696/706/Active site: Cys #status predicted

Query Match 14.5%; Score 155; DB 1; Length 1940;  
 Best Local Similarity 23.8%; Pred. NO. 0.34;  
 Matches 53; Conservative 51; Mismatches 83; Gaps 7;

QY	24	LKRLDLNVRQLOSONKOKERKDYSIITDLRPLUENNAATVYSLOALGKAEMLCSTLKQ	83
		: : : : :   : : : : :   : : : : :   : : : : :	
Db	1204	LAEDIDNLOVRKOKLERSEFLIEDIDSSVE-----SVSKANLEKICRTLEDQ	1256
QY	84	MKYLEQOQDETKOA-----OEAGRLSKMKKTMEQIELL-----OSQLPEVEEM	128
		: : : : :   : : : : :   : : : : :   : : : : :	
Db	1257	LSEKRGKNEETQOSSLSELTTQKSRLOTGEGELSRQLEEKESTVSOSSKQAF7QOQIEEL	1316
QY	129	IRDMGVQSASVEQALAVY-----CVSLKEKENLKEARKASGEVADRLKRLDEFSRSKL	181
		: : : : :   : : : : :   : : : : :   : : : : :	
Db	1317	KROLFEENKKNMLNLAHLOSRRHDCOLLKEDQYEEDEGEGAEIQLRLSKANSEVAOMRTKY	1376
QY	182	QT-----VYSELDAQLELKSACKDLOSADKREIMSLKKLTMLQ	220

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      :| ||::|| :| ||: || ::::: :| :| :
Db 1377 ETDAIQRTTEELFAKKL--AQR-LQDSEEQVEAVNAKCASTLE 1416

```

RESULT 18

myosin heavy chain II - Acanthamoeba castellanii  
 N:Contains: myosin ATPase (EC 3.6.1.32)  
 C:Species: Acanthamoeba castellanii  
 C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 19-Jan-2001  
 C:Accession: A27224  
 R:Hammer III, J.A.; Bowers, B.; Paterson, B.M.; Korn, E.D.  
 J. Cell Biol. 105, 913-925, 1997  
 A:Title: Complete nucleotide sequence and deduced polypeptide sequence of a nonmuscle  
 A:Reference number: A27224; MUID:87308395  
 A:Accession: A27224  
 A:Molecule type: DNA  
 A:Residues: 1-1509 <RAM>  
 A:Cross-references: GB:Y00624; GB:M12702; GB:M12703; GB:M19549; NID:g5585; PIDN:CA68  
 C:Genetics:  
 A:Introns: 69/3; 119/3; 181/2  
 C:Superfamily: myosin heavy chain; myosin motor domain homology  
 C:Keywords: actin binding; ATP; coiled coil; hydrolyase; methylated amino acid; nucleoe  
 F:92-775/Domain: myosin motor domain homology <MOM>  
 F:187-189/Region: nucleotide-binding motif A (P-loop)  
 F:544-576/Region: actin binding #Status predicted  
 F:660-682/Region: actin binding #Status predicted  
 F:848-1227/Domain: coiled coil #status predicted <OI>  
 F:1228-1247/Domain: hinge <HIN>  
 F:1248-1482/Domain: coiled coil #status predicted <CO2>  
 F:1483-1509/Domain: carboxyl-terminal <CBT>  
 F:133/Modified site: N6,N6,N6-trimethyllysine (lys) #status predicted  
 F:188/Binding site: ATP (lys) #status predicted

Query Match	14.5%	Score 154.5;	DB 1;	Length 1509;
Best Local Similarity	25.8%	Pred. No. 0.28;		
Matches 69; Conservative	52;	Mismatches 91;	Indels 55;	Gaps 7;

Oy		5	NKLFEDILAEENVLDEEFLKNGLDWNVAOLSKO-----KEKRPSQ	46
			: :     : : : :   : : : :   : :	:
Dd		894	DKLEKDAAALKIKLLIDEGRKADLEDNALLOKKVAGLEEELQEETSASNDILEGRKRL	953
			: : : : : : : : : : : : : : : : : :	:
Oy		47	VIIDLRDTLEERNATVVSLOALGRAE-----MLCSTLKQKMVKYEOOD	92
			: : :   :   : : : : : : : : : : : : : :	:
Dd		954	AENGSLAALLEERNNRKAQLQAETKYESBERNLDPJEDEAHADSLKKREEDLSREL	1013
			: : : : : : : : : : : : : : : : : :	:
Oy		93	ETXKOABEAGR---LBSKKTMEQLLEILLQSUPREV-BEMIRMDGVGOSAVEQCLAVYC	147
			: :   : :   : : : : : : : : : : : :	:
Dd		1014	ETKOLLDAENISSETLSKLTKMTERADDVRINDLDVTFKIQLTERTKSLEEBELAOTRA	1073
			: : : : : : : : : : : : : : : : : :	:
Oy		148	SUKREYNLTKEARKAGEVDVLNRKDLFFSRSSLOTWYSELDQARLETSAQ--KDO-	203
			: : :   : : : : : : : : : : : : : : : :	:
Dd		1074	QLEBE----KSQRKAASRSKAKQGOOLEARSSEVDSLKLSLAERKSLTKTDQORULDE	1129
			: : : : : : : : : : : : : : : : : :	:
Oy		204	-----SADKETMSLKKULTMQ	220
			: : : : : : : : : : : : : : : : : :	:
Dd		1130	QLEBERTVANWDROKKALEFAEKLTJELE	1156
			: : : : : : : : : : : : : : : : : :	:

## RESULT 19

Chromosome segregation protein (smc1) PA22109 - Pyrococcus abyssi (strain Orlay)  
C:Species: Pyrococcus abyssi  
C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000  
C:Accession: B75150  
R:anonymous; GenomeScope  
submitted to the EMBL Data Library, July 1999  
A:Description: Pyrococcus abyssi genome sequence: Insights into archaeal chromosome s  
A:Reference number: A75001  
A:Accession: B75150  
A:Status: preliminary  
A:Molecule type: DNA



A:Residues: 1-1177 <KAM>  
A:CROSS-references: GB:A1248284, GB:A1096836, NID:g5457730, PIDN:CA649281.1, PID:g5457799  
A:Experimental source: strain Orsay  
C:Genetics:  
A:Gene: PAB2109  
C:Superfamily: chromosome segregation protein SKC1

Query Match	14.4%;	Score 154;	DB 2;	length 1177;
Best Local Similarity	22.9%;	Pred. No. 0.23;		
Matches	57;	Conservative	61;	Mismatches 87;
				Indels 44;
				Gaps 10;

[illegible]

```

RESULT 20
T22976
hypothetical protein F59A2.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
R:Accession: T22976; T23157
R:Lightning, J
submitted to the EMBL Data Library, June 1994
A:Reference number: Z19645
A:Accession: T22976
A:Molecule type: DNA
A:Status: preliminary; translated from GR/EMBL/DBDJ
A:Residues: 1-1133 <MIL>
A:Cross-references: EMBL:Z34801; PIDN:CAA84332.1; GSPDB:GN00021; CESP:F59A2.6
A:Experimental source: clone F59A2
R:Burton, J.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z19700
A:Accession: T23157
A:Status: preliminary; translated from GR/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1133 <M12>
A:Cross-references: EMBL:Z66514; PIDN:CAA91344.1; GSPDB:GN00021; CESP:F59A2.6
A:Experimental source: clone K01A11
C:Genetics:
A:Gene: CESP:F59A2.6
A:Map position: 3
A:Introns: 13/2; 43/3; 107/3; 413/3; 492/3; 567/3; 635/3; 710/3; 738/3; 795/2; 1008/3; 1

```

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Query Match      14.4%  Score 153.5;  DB 2;  Length 1133;
Best Local Similarity 25.0%;  Pred. No. 0.24;
Matches 60;  Conservative 62;  Mismatches 77;  Indels 41;  Gaps 10;

QY  13 QEEENVL--DREFTLNEDNVRAQLSOKDKERDS-QYIIFLRDLTEERNATVS----- 65
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db   93 ESKKVLESEKQAFENKEQEREDLAKAMELNSEQNIILDEVTKKLQSESEVYLAAGA 152
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::

QY  66 ---LQALGKAEMLCSTLKKMKYILEQOODETKQAQEEAGRLSRKMTM-----EQ 113
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::

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Db 153 IQELTKEESEKETRSTAKTLEAVSKKLDSEERSLKFEFSDMI EAMK IOLI INEKQDEA 212
O7 114 IELLQSOGLPVEEEMIBMGVO-----SAVEOLAVYCVSLKREYMLKPKRARSCE 165
213 VELLQO--KLEEEKMSDVEYOKOLLLESTTSSEKKOHAEEAETVKO---LEEQSS---265
O7 166 VADKLKDLFFSRSKLOTVY-----SELDQAKLELKSQKQDLQSDAKIEIMSLKKLMTLO 220
Db 266 -IENLKQAEMERN-LKTALESDESSAISETTKOMEAKKELVASEKESKELSEEDQORLO 323

```

## RESULT 21

160K golgi antigen - human (fragment)

C:\Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 21-Jul-2000

R;Fritzler, M.J.; Hamel, J.C.; Ochs, R.L.; Chan, E.K.L.  
 J Exp Med 178 49-52 1993

A;Title: Molecular characterization of two  
A;Reference number: JH0820: MMRD:93301617

A:Accession: JH0820  
A:Molecule type: MR

A;residues: 1-579 <FR1>  
A;Cross-references: EMBL:L06148: NID:q306783: PIDN:AAA35921.1: PID:q553309

A/Note: this protein has alpha-helical structure with beta sheet regions

F;67-73/Region: proline-rich

F;419-455/Region: leucine zipper motif

Query Match	14.3%	Score 152.5;	DB 2;	Length 579;
Best Local Similarity	25.0%;	Pred. No. 0.13;		
Matches 55;	Conservative 42;	Mismatches 86;	Indels 37;	Gaps 6

[illegible]

RESULT 22

myosin beta heavy chain, cardiac and skeletal muscle - human

C;Species: Homo sapiens (man)

C;Accession: A37102; S12733; A94224; B28908; A24997; A27858; I54254; S12458  
R:Jaenicke T : Diederich K W : Haas W : Gleich I : Richter P : Pford

**A:Title:** The complete sequence of the human beta-myosin heavy chain gene and a comparison

A:Accession: A37102  
A;Reference number: A3/102; MUID:91065634

A;Molecule type: DNA  
A;Residues: 1-1935

R;Liew, C.C.; Sole, M.J.; Yamauchi-Takihara, K.; Kellam, B.; Anderson, D.H.; Lin, L.; A/Cross References. GB:MJ/50J, MID.gj/550/, FIDN:AAAC103/.1, FID.gj/5500, A/Cross References. GB:MJ/50J, MID.gj/550/, FIDN:AAAC103/.1, FID.gj/5500,

A; Title: Complete sequence and organization of the human cardiac beta-myosin heavy ch

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A:Accession: S12733  
 A:Molecule type: DNA  
 A:Residues: 1-106, 'E', 108-671, 'LVH', 675-857, 'A', 859-941, 'NV', 944-1123, 'A', 1125-1158, 'C',  
 A:Cross-references: EMBL:X82869; NID:929726; PIDN:CAA37068.1; PID:929727  
 R:Iamach-Takahara, K.; Sole, M.J.; Liew, J.; Ing, D.; Liew, C.C.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 3504-3508, 1989  
 A:Title: Characterization of human cardiac myosin heavy chain genes.  
 A:Reference number: A94224; MUID:89264452  
 A:Accession: A94224  
 A:Molecule type: DNA  
 A:Residues: 1-87, 'Q', 89-106, 'E', 108-177, 1325-1702, 'DR', 1705-1786, 1788-1803, 'E', 1804-1935  
 R:Yamauchi-Takahara, K.; Sole, M.J.; Liew, J.; Ing, D.; Liew, C.C.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 7416-7417, 1989  
 A:Reference number: A94226  
 A:Contents: annotation; erratum  
 R:Kurabayashi, M.; Tsuchimochi, H.; Komuro, I.; Takaku, F.; Yazaki, Y.  
 J. Clin. Invest. 82, 524-531, 1988  
 A:Title: Molecular cloning and characterization of human cardiac alpha- and beta-form my  
 human atrium.  
 A:Reference number: A92770; MUID:88299163  
 A:Accession: B28908  
 A:Molecule type: mRNA  
 A:Residues: 1412-1518, 'R', 1520-1574, 'NV', 1577-1935 <KUR>  
 A:Cross-references: GB:M21665  
 A:Note: the authors translated the codon AGC for residue 108 as Arg  
 R:Uchler, P.; Umeda, P.K.; Levin, J.E.; Vosberg, H.P.  
 Eur. J. Biochem. 160, 419-426, 1986  
 A:Title: Partial characterization of the human beta-myosin heavy-chain gene which is exp  
 A:Reference number: A24997; MUID:87030293  
 A:Accession: A24997  
 A:Molecule type: DNA  
 A:Residues: 682-721, 975-1112, 1854-1935 <LIC>  
 A:Cross-references: GB:X04627  
 R:Seiz, L.J.; Gianola, K.M.; McNally, E.M.; Feghall, R.; Eddy, R.; Shows, T.B.; Leinwand  
 Nucleic Acids Res. 15, 5443-5459, 1987  
 A:Title: Human cardiac myosin heavy chain genes and their linkage in the genome.  
 A:Reference number: A93669; MUID:87260010  
 A:Accession: A27858  
 A:Molecule type: DNA  
 A:Residues: 1854-1865, 'A', 1867-1935 <SAE>  
 A:Cross-references: GB:X05631; GB:Y00362; NID:934643; PIDN:CAA29119.1; PID:934644  
 R:Diederich, K.W.; Eisele, I.; Red, T.; Jeneicke, T.; Lichter, P.; Vosberg, H.P.  
 Hum. Genet. 81, 214-220, 1989  
 A:Title: Isolation and characterization of the complete human beta-myosin heavy chain ge  
 A:Reference number: I54254; MUID:89154425  
 A:Accession: I54254  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 653-720 <RES>  
 A:Cross-references: GB:M27636; NID:9179511; PIDN:AAA79019.1; PID:9601916  
 R:Bober, E.  
 submitted to the EMBL Data Library, January 1989  
 A:Reference number: S12458  
 A:Accession: S12458  
 A:Molecule type: mRNA  
 A:Residues: 785-1076, 'E', 1078-1123, 'A', 1125-1702, 'DE', 1705-1935 <BOB>  
 A:Cross-references: EMBL:X51591; NID:929467; PIDN:CAA35940.1; PID:929468  
 R:Bober, E.; Buchberger-Seidl, A.; Braun, T.; Singh, S.; Goede, H.W.; Arnold, H.H.  
 Eur. J. Biochem. 189, 55-65, 1990  
 A:Title: Identification of three developmentally controlled isoforms of human myosin hea  
 A:Reference number: S09331; MUID:90235862  
 A:Accession: S09331  
 A:Molecule type: mRNA  
 A:Residues: 785-830, 'X', 833-900, 'X', 902-970, 'X', 972-1040, 'X', 1042-1076, 'E', 1078-1110, 'X',  
 '1602-1670, 'X', 1672-1702, 'DE', 1705-1740, 'X', 1742-1810, 'X', 1812-1935 <BOB>  
 A:Cross-references: EMBL:X51591  
 R:Jandreski, M.A.; Liew, C.C.  
 Hum. Genet. 76, 47-53, 1987  
 A:Title: Construction of a human ventricular cDNA library and characterization of a beta  
 A:Reference number: S02229; MUID:87152738  
 A:Accession: S02229  
 A:Molecule type: mRNA  
 A:Residues: 1393-1702, 'DR', 1705-1935 <JAN>

A:Cross-references: EMBL:X06976; NID:934860; PIDN:CAA30039.1; PID:9825694  
 R:Seiz, L.; Leinwand, L.A.  
 Nucleic Acids Res. 14, 2951-2969, 1986  
 A:Title: Characterization of diverse forms of myosin heavy chain expressed in adult h  
 A:Reference number: A93616; MUID:8616778  
 A:Accession: B23767  
 A:Molecule type: mRNA  
 A:Residues: 1131-1312, 'G', 1314-1355, 'R', 1357-1358, 'GD', 1361-1438, 'LQ', 14  
 A:Note: the first ten codons of the sequence figure show the reverse complementary st  
 C:Genetics:  
 A:Gene: GDB:MYH7  
 A:Cross-references: GDB:120215; OMIM:160760  
 A:Map position: 14q12-14q12  
 A:Introns: 67/3: 115/3: 168/1: 177/2: 213/3: 244/3: 266/1: 299/1: 333/3: 380/1: 419/3  
 24/3: 1390/2: 1451/3: 1507/1: 1548/3: 1651/3: 1719/3: 1761/3: 1853/3: 1885/3: 1930/3  
 C:Superfamily: myosin heavy chain; myosin motor domain homology  
 C:Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; hydrolase; methyl  
 F:88-766/Domain: myosin motor domain homology <CMOT>  
 F:178-185/Region: nucleotide-binding motif A (P-loop)  
 F:548-585/Region: actin binding #status predicted  
 F:655-677/Region: actin binding #status predicted  
 F:839-1935/Domain: coiled coil #status predicted <COIL>  
 F:839-1279/Region: S2  
 F:1280-1935/Region: light meromyosin  
 F:129/Modified site: N6, N6, N6-trimethyllysine (Lys) #status predicted  
 F:184/Binding site: ATP (Lys) #status predicted  
 F:655,705/Active site: Cys #status predicted

Query Match 14.3%; Score 152.5; DB 1; Length 1935;  
 Best Local Similarity 20.5%; Pred. No. 0.47;  
 Matches 61; Conservative 60; Mismatches 88; Indels 89; Gaps 9;

```

QY 1 RTINKFPEDLAEEENVLDL-----EFIK----- 25
      || |||||:|:|
Db 1129 RAKVEKRLSDLSRELEISRLFEAGCATSVQIEMNKREAFQKMRDLEATLQHEAT 1188
      |||||:|:|
QY 26 -----NELNVRQAQSQKDKERKDSVITDITLDITLEENATVLSQQA 69
      |||||:|:|
Db 1189 AALRKKNHADSVAELGQIDNLDQVKKLEKSEFLELDIVNSNMQ-----ITKA 1241
      |||||:|:|
QY 70 LGKAEMLCSTLKQKMYLEQOODETKQAEAGRLRSKMT-----MEQIELLSQ 121
      |||||:|:|
Db 1242 KANLEKKCRITLEDQNMNHRKAEFTQSVNDLTSQRAKLTQENELSRDLDEKALISQ 1300
      |||||:|:|
QY 122 LP-----EVEDMITDMGVGSAAVEQLAAVYCSLKREYNLEKARKASGEV 166
      |||||:|:|
Db 1301 LTRGKLTYYTOQLDLKRLQLEEEVAKKALAHALQASARHDCDLREQYEETFEAKAEQLRV 1360
      |||||:|:|
QY 167 ADKIRKDLFFSSRSKLTQ-----VSELDQAKTELKSAQKDLQSAKDEIMSLKKKLTMLQ 220
      |||||:|:|
Db 1361 LSKANSEVAQWRKYETDAIQRTELEAKKLT--AQR-LQEAEEAVEAVNAKCSLE 1415
      |||||:|:|

```

RESULT 23  
 S21801  
 myosin heavy chain, neuronal [similarity] - rat  
 N:Alternate names: myosin II  
 N:Contains: myosin ATPase (EC 3.6.1.32)  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 31-Dec-1993 #sequence, revision 31-Dec-1993 #text\_change 19-Jan-2001  
 C:Accession: S21801; PNO013; S18134  
 R:Sun, W.; Chantler, P.D.  
 J. Mol. Biol. 224, 1185-1193, 1992  
 A:Title: Cloning of the cDNA encoding a neuronal myosin heavy chain from mammalian br  
 A:Reference number: S21801; MUID:92235856  
 A:Accession: S21801  
 A:Molecule type: mRNA  
 A:Residues: 1-1999 <SUN>  
 A:Cross-references: EMBL:X62659  
 R:Sun, W.; Chantler, P.D.  
 Biochem. Biophys. Res. Commun. 175, 244-249, 1991  
 A:Title: A unique cellular myosin II exhibiting differential expression in the cerebr

A:Reference number: PNO013; MUID:91151356  
A:Accession: PNO013  
A:Molecule type: mRNA  
A:Residues: 1914-1998, 'I' <SU2>  
A:Experimental source: brain  
C:Superfamily: myosin heavy chain; myosin motor domain homology  
C:Keywords: actin binding; ATP; coiled coil; hydrolyase; methylated amino acid; nucleotide  
F:84-763/Domain: myosin motor domain homology <MMOT>  
F:174-181/Region: nucleotide-binding motif A (P-loop)  
F:541-575/Region: actin binding #status predicted  
F:653-675/Region: actin binding #status predicted  
F:836-1999/Domain: coiled coil #status predicted <COI>  
F:127-1999/Region: light meromyosin  
F:125/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted  
F:180/Binding site: ATP (Lys) #status predicted  
F:693,703/Active site: Cys #status predicted  
F:1916/Binding site: phosphate (Ser) (covalent) #status predicted  
F:1943/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 14.3% Score 152.5; DB 1; Length 1999;  
Best Local Similarity 20.7% Pred. No. 0.49;  
Matches 54; Conservative 54; Mismatches 88; Indels 65; Gaps 6;  
QY 11 LAOEENVLDRREF-----LNELDNVRAQLSOKDKERDSQVITDRLDTL 56  
Db 1088 LARVEEAQNMALMKTIRELESQISELDLESRAARNKAKOKRLGDELEAKTEL 1147  
QY 57 EERNATVSLQALGKAEMLCSTLKKOM-----KYLEQOODETKQA 97  
Db 1148 ELDLDTSTAQOELIRSKRQEVNILLKLTLEEAQTHQAIOEMRKHSQAVEELARQL 1207  
QY 98 QOEGRILSKKTKMT-----QIELLOS-----QLEPEVEIRMGV-----GQSAV 139  
Db 1208 KRKAANLEKAKOTLENERGELANEKVKVLLQGRDSEHNRKRYEAOLEQVFNENGERRV 1267  
QY 140 EQLAIVCYSLKKEYENLEKARKAGEVADKLKDLFSRSKLOQVYSELDAQLELKSAQ 199  
Db 1268 TELADKTVKRLQVELDNVGLSOSDSKSKLTKDPSALESQLQ-----DTQ 1313  
QY 200 KDLQADKEIMSLKKKRLTMQ 220  
Db 1314 ELLOEENRQKLSLSTFKQVE 1334

RESULT 24  
C35815  
myosin heavy chain 3, muscle - fruit fly (Drosophila melanogaster) (fragment)  
C:Species: Drosophila melanogaster  
C:Date: 28-Mar-1991 #sequence\_revision 28-Mar-1991 #text\_change 20-Jun-2000  
R:Collier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.  
Genes Dev. 4, 885-895, 1990  
A:Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion that  
A:Reference number: A35815; MUID:90346288  
A:Accession: C35815  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1175 <COL>  
A:Cross-references: EMBL:X53155; NID:98219; PIDN:CAA37308.1; PID:92546936  
A:Note: the authors translated the codon TGC for residue 649 as Lys, and AAG for residue  
C:Genetics:  
A:Gene: FlyBase:Mhc  
A:Cross-references: FlyBase:Fbgn0002741  
C:Superfamily: myosin heavy chain; myosin motor domain homology  
C:Keywords: ATP

Query Match 14.3% Score 152; DB 2; Length 1175;  
Best Local Similarity 23.9% Pred. No. 0.3;  
Matches 62; Conservative 49; Mismatches 84; Indels 64; Gaps 9;

QY 11 LAOEENVLDRREFLNELDNVRAQLSOKDKER-----RDSQVITDRLDTLE----- 57  
Db 789 LEOENKVLARQL---ELSOVRQELDRIRIQKEEFENTKRNHQRALDSMQASLEAKG 845  
QY 58 -----ERNATVSLQALGKAEMLCSTLKKOMKYLEQOODETKQAQOEAGRLSKM 108  
Db 846 KAEALRMKKKLEADINLEIALDHANKANAEAKNIRYQOOLDIQALDEEQRARDA 905  
QY 109 KTMQDIEL-----LLOSQLEPEVEEMIRDMQVGSQAVQLAVYCVSLKKEYENLEKARKA 162  
Db 906 R--EOLGISERRANALONELESRTLLLEQADGRGROAQ-----ELADAHQLENVSAQ 957  
QY 163 SGEVADKLKRLDFFSRSKLOQVYSELDO-----AKL--ELKSAQKD 201  
Db 958 NASISAAKRR---LESELQTLHSDLDLLEAKNSEKAKKANVDAARLADLRADQDH 1013  
QY 202 LQSAADKEIMSLKKKRLTMQ 220  
Db 1014 AQTQEKRLKALQEQIQKEIQ 1032

RESULT 25  
D35815  
myosin heavy chain 4, muscle - fruit fly (Drosophila melanogaster) (fragment)  
C:Species: Drosophila melanogaster  
C:Date: 28-Mar-1991 #sequence\_revision 28-Mar-1991 #text\_change 13-Feb-1998  
C:Accession: D35815  
R:Collier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.  
Genes Dev. 4, 885-895, 1990  
A:Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion t  
A:Reference number: A35815; MUID:90346288  
A:Accession: D35815  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1175 <COL>  
A:Cross-references: EMBL:X53155  
A:Note: the authors translated the codon TGC for residue 649 as Lys, and AAG for resi  
C:Genetics:  
A:Gene: FlyBase:Mhc  
A:Cross-references: FlyBase:Fbgn0002741  
C:Superfamily: myosin heavy chain; myosin motor domain homology  
C:Keywords: ATP

Query Match 14.3% Score 152; DB 2; Length 1175;  
Best Local Similarity 23.9% Pred. No. 0.3;  
Matches 62; Conservative 49; Mismatches 84; Indels 64; Gaps 9;  
QY 11 LAOEENVLDRREFLNELDNVRAQLSOKDKER-----RDSQVITDRLDTLE----- 57  
Db 789 LEOENKVLARQL---ELSOVRQELDRIRIQKEEFENTKRNHQRALDSMQASLEAKG 845  
QY 58 -----ERNATVSLQALGKAEMLCSTLKKOMKYLEQOODETKQAQOEAGRLSKM 108  
Db 846 KAEALRMKKKLEADINLEIALDHANKANAEAKNIRYQOOLDIQALDEEQRARDA 905  
QY 109 KTMQDIEL-----LLOSQLEPEVEEMIRDMQVGSQAVQLAVYCVSLKKEYENLEKARKA 162  
Db 906 R--EOLGISERRANALONELESRTLLLEQADGRGROAQ-----ELADAHQLENVSAQ 957  
QY 163 SGEVADKLKRLDFFSRSKLOQVYSELDO-----AKL--ELKSAQKD 201  
Db 958 NASISAAKRR---LESELQTLHSDLDLLEAKNSEKAKKANVDAARLADLRADQDH 1013  
QY 202 LQSAADKEIMSLKKKRLTMQ 220  
Db 1014 AQTQEKRLKALQEQIQKEIQ 1032

RESULT 26  
A35815  
myosin heavy chain 1, muscle - fruit fly (Drosophila melanogaster) (fragment)  
C:Species: Drosophila melanogaster

C>Date: 12-Oct-1990 #sequence\_revision 28-Mar-1991 #text\_change 20-Jun-2000  
 C:Accession: A35815  
 R:Collier, V.L.; Kromert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.  
 Genes Dev. 4, 885-895, 1990  
 A:Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion that  
 A:Reference number: A35815; MUID:90346288  
 A:Accession: A35815  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1201 <COL>  
 A:Cross-references: EMBL:X53155; NID:98219; PIDN:CAA37310.1; PID:92546938  
 A>Note: the authors translated the codon TGC for residue 649 as Lys, and AAG for residue  
 C:Genetics:  
 A:Gene: FlyBase:Mhc  
 A:Cross-references: FlyBase:FBgn0002741  
 C:Superfamily: myosin heavy chain; myosin motor domain homology  
 C:Keywords: ATP

Query Match 14.3%; Score 152; DB 2; Length 1201;  
 Best Local Similarity 23.9%; Pred. No. 0.31;  
 Matches 62; Conservative 49; Mismatches 84; Indels 64; Gaps 9;  
 QY 11 LAOEENVLDREFLNELDNVRAOLSOQDKRK-----RDSQVIIDTLRDTLE----- 57  
 Db 789 LEOENKVLRAQL---ELSQVROEIDRRIOKEEPEENTRNHQRALDSMQASLEAEAKG 845  
 QY 58 -----ERNATVSLQALGKAEMLCSTLKKOMKYLEQOODETQAOEAGRLRSKM 108  
 Db 846 KAELRMKKKLEADINELEIALDHANKANAEQKNIRYQOQLDIOTALEEQRARDDA 905  
 QY 109 KTMEOIEL-----LQSOLPEVEEMIRDMGVGSAVEQLAVCVSLKEVENLKEARKA 162  
 Db 906 R--EQGISERRANALQNELESRTLLLEQADRGRRQAEQ-----ELADAHQOLNEVSAQ 957  
 QY 163 SGEVADKLKLDLSSRSKLTQTVSELDQ-----AKT--ELKSAQKD 201  
 Db 958 NASISAAKRR---LESELQTLHSDLDLDELNEAKNSEKAKKAWDAARLADLRAEQDH 1013  
 QY 202 LOSADKEIMSLKKRLTMQ 220  
 Db 1014 AQTOEKLKRALEQOIKELQ 1032

RESULT 27  
 B35815  
 myosin heavy chain 2, muscle - fruit fly (Drosophila melanogaster) (fragment)  
 C:Species: Drosophila melanogaster  
 C>Date: 28-Mar-1991 #sequence\_revision 28-Mar-1991 #text\_change 20-Jun-2000  
 C:Accession: B35815  
 R:Collier, V.L.; Kromert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.  
 Genes Dev. 4, 885-895, 1990  
 A:Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion that  
 A:Reference number: A35815; MUID:90346288  
 A:Accession: B35815  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1201 <COL>  
 A:Cross-references: EMBL:X53155; NID:98219; PIDN:CAA37311.1; PID:92546939  
 A>Note: the authors translated the codon TGC for residue 649 as Lys, and AAG for residue  
 C:Genetics:  
 A:Gene: FlyBase:Mhc  
 A:Cross-references: FlyBase:FBgn0002741  
 C:Superfamily: myosin heavy chain; myosin motor domain homology  
 C:Keywords: ATP

Query Match 14.3%; Score 152; DB 2; Length 1201;  
 Best Local Similarity 23.9%; Pred. No. 0.31;  
 Matches 62; Conservative 49; Mismatches 84; Indels 64; Gaps 9;  
 QY 11 LAOEENVLDREFLNELDNVRAOLSOQDKRK-----RDSQVIIDTLRDTLE----- 57  
 Db 1014 AQTOEKLKRALEQOIKELQ 1032

Db 789 LEOENKVLRAQL---ELSQVROEIDRRIOKEEPEENTRNHQRALDSMQASLEAEAKG 845  
 QY 58 -----ERNATVSLQALGKAEMLCSTLKKOMKYLEQOODETQAOEAGRLRSKM 108  
 Db 846 KAELRMKKKLEADINELEIALDHANKANAEQKNIRYQOQLDIOTALEEQRARDDA 905  
 QY 109 KTMEOIEL-----LQSOLPEVEEMIRDMGVGSAVEQLAVCVSLKEVENLKEARKA 162  
 Db 906 R--EQGISERRANALQNELESRTLLLEQADRGRRQAEQ-----ELADAHQOLNEVSAQ 957  
 QY 163 SGEVADKLKLDLSSRSKLTQTVSELDQ-----AKT--ELKSAQKD 201  
 Db 958 NASISAAKRR---LESELQTLHSDLDLDELNEAKNSEKAKKAWDAARLADLRAEQDH 1013  
 QY 202 LOSADKEIMSLKKRLTMQ 220  
 Db 1014 AQTOEKLKRALEQOIKELQ 1032

RESULT 28  
 A32491  
 myosin heavy chain 1, muscle - fruit fly (Drosophila melanogaster)  
 C:Species: Drosophila melanogaster  
 C>Date: 12-Oct-1989 #sequence\_revision 31-Dec-1993 #text\_change 02-Feb-2001  
 C:Accession: A32491  
 R:George, E.L.; Ober, M.B.; Emerson Jr., C.P.  
 Mol. Cell. Biol. 9, 2957-2974, 1989  
 A:Title: Functional domains of the Drosophila melanogaster muscle myosin heavy-chain  
 A:Reference number: A32491; MUID:89364536  
 A:Accession: A32491  
 A>Status: preliminary  
 A:Molecule type: DNA; mRNA  
 A:Residues: 1-2385 <GEO>  
 A:Cross-references: GB:M61229; GB:M27194  
 A>Note: the authors translated the codon TGC for residue 329 as Ser  
 C:Genetics:  
 A:Gene: FlyBase:Mhc  
 A:Cross-references: FlyBase:FBgn0002741  
 C:Superfamily: myosin heavy chain; myosin motor domain homology  
 C:Keywords: ATP; nucleotide binding; P-loop  
 F:157-1032/Domain: myosin motor domain homology #status atypical <MMO>  
 F:227-234/Region: nucleotide-binding motif A (P-loop)

Query Match 14.3%; Score 152; DB 2; Length 2385;  
 Best Local Similarity 23.9%; Pred. No. 0.63;  
 Matches 62; Conservative 49; Mismatches 84; Indels 64; Gaps 9;  
 QY 11 LAOEENVLDREFLNELDNVRAOLSOQDKRK-----RDSQVIIDTLRDTLE----- 57  
 Db 1999 LEOENKVLRAQL---ELSQVROEIDRRIOKEEPEENTRNHQRALDSMQASLEAEAKG 2055  
 QY 58 -----ERNATVSLQALGKAEMLCSTLKKOMKYLEQOODETQAOEAGRLRSKM 108  
 Db 2056 KAELRMKKKLEADINELEIALDHANKANAEQKNIRYQOQLDIOTALEEQRARDDA 2115  
 QY 109 KTMEOIEL-----LQSOLPEVEEMIRDMGVGSAVEQLAVCVSLKEVENLKEARKA 162  
 Db 2116 R--EQGISERRANALQNELESRTLLLEQADRGRRQAEQ-----ELADAHQOLNEVSAQ 2167  
 QY 163 SGEVADKLKLDLSSRSKLTQTVSELDQ-----AKT--ELKSAQKD 201  
 Db 2168 NASISAAKRR---LESELQTLHSDLDLDELNEAKNSEKAKKAWDAARLADLRAEQDH 2223  
 QY 202 LOSADKEIMSLKKRLTMQ 220  
 Db 2224 AQTOEKLKRALEQOIKELQ 2242

RESULT 29  
 B32491  
 myosin heavy chain 2, muscle - fruit fly (Drosophila melanogaster)  
 C:Species: Drosophila melanogaster

C>Date: 12-Oct-1989 #sequence\_revision 31-Dec-1993 #text\_change 02-Feb-2001  
 C/Accession: B32491  
 R:George, E.L.; Ober, M.B.; Emerson Jr., C.P.  
 Mol. Cell. Biol. 9, 2957-2974, 1989  
 A>Title: Functional domains of the Drosophila melanogaster muscle myosin heavy-chain gene  
 A/Reference number: A32491; MUID:89384556  
 A/Accession: B32491  
 A>Status: preliminary  
 A:Molecule type: DNA: mRNA  
 A:Residues: 1-2411 <GEO>  
 A:Cross-references: GB:M61229; GB:M71194  
 A>Note: the authors translated the codon TGC for residue 329 as Ser  
 C/Genetics:  
 A:Gene: FlyBase:Mhc  
 A:Cross-references: FlyBase:FBgn0002741  
 C:Superfamily: myosin heavy chain; myosin motor domain homology  
 C/Keywords: ATP; nucleotide binding; P-loop  
 F:137-1032/Domain: myosin motor domain homology #status atypical <MMO>  
 F:227-234/Region: nucleotide-binding motif A (P-loop)

Query Match 14.3%; Score 152; DB 2; Length 2411;  
 Best Local Similarity 23.9%; Pred. No. 0.63; Mismatches 84; Indels 64; Gaps 9;  
 Matches 62; Conservative 49; Mismatches 84; Indels 64; Gaps 9;  
 QY 11 LAQEEENVLDREPLKNEIDNVRAQLSOKDKKK-----RDSQVYIDTLRDITLE----- 57  
 Db 1999 LEQENKYLRAQL---ELSQVROELDRRIQKEEFENTRNHNRALDSMASLEAEKKG 2055  
 QY 58 -----ERNATVVSLOALGKAEMLCSTLKKOMKYLEQOODETKQAEAGRLRSKM 108  
 Db 2056 KAELRMKKLEADINLELEIALDHANKANAENAKNIRYQOQLDIQALBEEGRARDA 2115  
 QY 109 KTMQIEL-----LLOSQLEPEVEEMTRDMGVOSAVQALVYCVSLKKEENLKEAKKA 162  
 Db 2116 R-SQLGSERRANALQMLEESRTLEQADGRGRQABQ-----ELDAHEQUNEVSQ 2167  
 QY 163 SGEVADKLKRLDFSSRSKLTQVYSELQ-----AKL--ELKSAQKD 201  
 Db 2168 NASSISAKRK---LESLQTLHSDLDLDELLEAKNSEKAKKAWDARLADDELRAEDDH 2223  
 QY 202 LOSADKEIMSLKKRLTMLQ 220  
 Db 2224 AQTOEKLKRLAEQOIKEIQ 2242

## RESULT 30

T17272  
 hypothetical protein DKFZp434B0435.1 - human  
 C/Species: Homo sapiens (man)  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 01-Dec-2000  
 R:Postka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, September 1999  
 A/Reference number: Z18723  
 A/Accession: T17272  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1780 <POD>  
 A:Cross-references: EMBL:AL117496  
 A:Experimental source: adult testis; clone DKFZp434B0435  
 R:Ansorge, W.; Wiltner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, January 2000  
 A/Reference number: Z23028  
 A/Accession: T46451  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 575-1136, 'C', 1138-1608, 'K', 1610-1780 <AAA>  
 A:Cross-references: EMBL:AL137392  
 A:Experimental source: adult testis; clone DKFZp434I152  
 R:Westendorf, J.M.; Rao, P.N.; Gerace, L.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 714-718, 1994  
 A>Title: Cloning of cDNAs for M-phase phosphoproteins recognized by the MPW2 monoclonal

A/Reference number: A36881; MUID:94119956  
 A/Accession: A36881  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1215-1261, 'E', 1263-1418, 'S', 1420-1608, 'K', 1610-1780 <WSS>  
 A:Cross-references: GB:L16782; NID:g292328; PIDN:AAC37542.1; PID:g292329  
 C/Genetics:  
 A>Note: DKFZp434B0435.1; DKFZp434I152.1  
 C/Keywords: phosphoprotein

Query Match 14.2%; Score 151.5; DB 2; Length 1780;  
 Best Local Similarity 21.3%; Pred. No. 0.49;  
 Matches 50; Conservative 62; Mismatches 84; Indels 39; Gaps 6;  
 QY 22 EFLKNEIDNVRAQL-SQKD-----KEK-----RDSQVYIDTLRDITLEERNAT----- 62  
 Db 1039 EELDQOIEKLOAEVKGKVDENNRLKEKHNKODDLKEKEETLLOQLKEELQEKVTLQVQ 1098  
 QY 63 --VVSLOALGKAEMLCSTLKKOMKYLEQOODETKQAEAGRLRSKMKTMEQIELLLQ 119  
 Db 1099 IQHVEGKRLSELTOGYTCYKAKIKELETLETKYKERSHSALEODILEKESTILKLE 1158  
 QY 120 SQLPEVEEMTRDMGVOSAVQALVYCVSLKKEEYNT-----KEARKASGE 165  
 Db 1159 RNLKEQFQHLQD---SVKNTKDLNVKLELKEEITQLTNNLDKMHLLQLKEEETNRQ 1215  
 QY 166 VADKLKRLDFSSRSKLTQVYSELQAKLELSAOKDLOSADKEIMSLKKRLTMLQ 220  
 Db 1216 ETEKLKEELSASSARTONLAKDLQKKEEDYADLEKELTLDAKKQIKQOKEVSVNR 1270

## RESULT 31

S54871  
 M protein - Streptococcus sp.  
 C/Species: Streptococcus sp.  
 C/Date: 08-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 26-Aug-1999  
 A/Accession: S54871  
 R:Podbielski, A.; Melzer, B.  
 submitted to the EMBL Data Library, June 1991  
 A/Reference number: S54871  
 A/Accession: S54871  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-532 <POD>  
 A:Cross-references: EMBL:X60097; NID:g840905; PIDN:CAAA2693.1; PID:g840906  
 C:Superfamily: M5 protein

Query Match 14.2%; Score 151; DB 2; Length 532;  
 Best Local Similarity 23.0%; Pred. No. 0.15; Mismatches 93; Indels 62; Gaps 8;  
 Matches 62; Conservative 52; Mismatches 93; Indels 62; Gaps 8;  
 QY 9 FDLAQOE-----EENVLDREPLK-----NELDNVRAQLS-----Q 37  
 Db 174 YDLIEELGKRLKENODLEKTKDKEFYLGTLRYINELDLKQLININDLKNELEQ 233  
 QY 38 KDKERQSOVYIDTLRDITLEERNATVVSLOALGKAEMLCSTLKKOMKYLEQOODETKQ 97  
 Db 234 KQKAEADQRT-LEAEKAKLEEEKQISDASRQSLRDLSDASREAKQOLEAEYOKLEEEKQI 292  
 QY 98 QEEAGR-LRSKMKTMEQIELLOSLPEVE-----MTRDMGVOSAVQALVY 145  
 Db 293 SDASRQSLRDLSDASREAKQOLEAEYOKLEEQNKITSEPSRGLRDLSDASREAKQOYBK 352  
 QY 146 CVSLKKEEYENLKEARKASGEVADKLKRLDFSSRSKLTQVYSELQAKLELSAQ---KDL 202  
 Db 353 LANITAEIDKYKEERQISDASRQSLRDLSDASREAKQOYKAEALAEANSKILAEKLEKEL 412  
 QY 203 QSADK-----EIMSLKKL 216  
 Db 413 EESKRLTEKEKAELOAKLEAEAKALKLEK 441

RESULT 32  
153799  
CGL protein - human  
C:Species: Homo sapiens (man)  
C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jul-2000  
C:Accession: I53799  
R:Print, C.G.; Leung, E.; Harrison, J.E.; Watson, J.D.; Krissansen, G.W.  
Gene 144, 221-228, 1994  
A:Title: Cloning of a gene encoding a human leukocyte protein characterised by extensive  
A:Reference number: I53799; MUID:94314220  
A:Accession: I53799  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1300 <RES>  
A:Cross-references: GB:I25616; NID:q409465; PIDN:AAB65853.1; PID:q409466  
C:Genetics:  
A:Gene: GDB:CG1  
A:Cross-references: GDB:450341

Query Match 14.2%; Score 151; DB 2; Length 1300;  
Best Local Similarity 26.6%; Pred. No. 0.38;  
Matches 67; Conservative 40; Mismatches 81; Indels 64; Gaps 11;

OY 10 DLAEENVLND--REFLNELDNVRAQLSOKD-----E 41  
DB 306 DLKESGVLDALKSSKSGELTLIHOLEKDLAAVKEDAAATDRCKQLTQEMMTE 365  
OY 42 KRDSQVIITLRLD--TLEE-----RNATVSLQALGKAMLCSTKKMKY---LEQQ 90  
DB 366 KERNVAVITRMKDRIGTLEKEHNVFNKIHVSQD-----TQGMKKFQGVREOM 415  
OY 91 QDETKAOEFGRLRSKM-KTMEIELLLOSQPEVEEMTRDQVGSQAVQLAVYCSL 149  
DB 416 EAETIAHLKQENGILRDVAVSNTNQL--SKQSAELNKLRLQDYA--RLVNELETKTGL 469  
OY 150 KKEYENLEKARKASGEVADLRKDLFSSRSKLTQVYSELDAKLELSAQKDLOS---A 205  
DB 470 QGEVQKKNNEQA---ATQLKVOLOEAEKRWEEVQSIKRTKRAHEPAQDLOSKEVAK 525  
OY 206 DKEIMSLKKLTL 217  
DB 526 ENEVQSLSKLT 537

RESULT 33  
S24348  
myosin heavy chain, embryonic and adult skeletal muscle (clone Cemb2) - chicken (fragment  
C:Species: Gallus gallus (chicken)  
C>Date: 03-Feb-1994 #sequence\_revision 06-Sep-1996 #text\_change 13-Feb-1998  
C:Accession: S24348  
R:Moore, L.A.; Arrisubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.  
J. Mol. Biol. 225, 1143-1151, 1992  
A:Title: Analysis of the chicken fast myosin heavy chain family. Localization of isoform  
A:Reference number: S24348; MUID:92309413  
A:Accession: S24348  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-955 <MOO>  
A:Cross-references: EMBL:M74085  
C:Superfamily: myosin heavy chain; myosin motor domain homology  
C:Keywords: ATP; coiled coil; muscle contraction; skeletal muscle; thick filament

Query Match 14.1%; Score 150.5; DB 2; Length 955;  
Best Local Similarity 23.9%; Pred. No. 0.29;  
Matches 56; Conservative 47; Mismatches 80; Indels 51; Gaps 8;

OY 24 LKNELDNVRAQLSOKDEKRDQVIITLRLTLEARNATVSLQALGKAMLCSTLKKQ 83  
DB 222 LGEOIDNLRVKOKLEKEKSELKMEIDDLASNME-----SVSKARANLEKMCRTLEDQ 274

OY 84 MKYLEQODE-----TKQA--OEAGRL-----RSKMKTEQIELL 117  
DB 275 LSKIKSKEEHEQRMINDLSTQRAQLTQESSEYSNOVEKDALISQSRGQAFQIIEEL 334  
OY 118 LQSLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEAR-----KASGEVAD- 168  
DB 335 KR-----HLEEFIRKAKNALAHALQSAHRDCDLRFQYEEQDEAKELQRLASKANSEVAQM 390  
OY 169 --KLRKLFSSRSKLTQVYSELDAKLELSAQKDLOSADKEIMSLKKLTLMLQ 220  
DB 391 RTKYETDAIGRTTELEAKKRLAQ--RLQDAEHEVAVNAKCAISLEKTRORLO 441

RESULT 34  
B70356  
chromosome assembly protein homolog - Aquifex aeolicus  
C:Species: Aquifex aeolicus  
C>Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 02-Jun-2000  
C:Accession: B70356  
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;  
V.  
Nature 392, 353-358, 1998  
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A:Reference number: A70300; MUID:98196666  
A:Accession: B70356  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1156 <AQF>  
A:Cross-references: GB:AE000699; NID:g2983238; PIDN:AAC06839.1; PID:g2983243; GB:AE00  
A:Experimental source: strain VF5  
C:Genetics:  
A:Gene: xcpC  
C:Superfamily: chromosome segregation protein SMCI

Query Match 14.1%; Score 150.5; DB 2; Length 1156;  
Best Local Similarity 23.6%; Pred. No. 0.36;  
Matches 52; Conservative 57; Mismatches 72; Indels 39; Gaps 9;

OY 11 LAQEEENVL-DREFLNELDNVRAQLSOKDEKRDQVIITLRLTLEARNATVSLQQA 69  
DB 232 LKKEKELKREKRIINLESLRESLDTITFQIODEKEKELERERLLKEVNEKIMPERK 291  
OY 70 LGR--AEMLCSTLKQKMYLEQODETKQAQEEAGRLRSKMKTEQIELLQSLPEVEE 127  
DB 292 VGKFTAE-----IENARSTIKEREKELKESENRYKNLE--LNNLLSKEN 336  
OY 128 MIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADLRKDLFSSRSKLTQVYSE 187  
DB 337 LEREVGLQLELEK-----LKREYSIKREVER-----EKLR-ELLEEEERLKITFDE 382  
OY 188 L-----DQAKI--ELKSAQKDLOSADKEIMSLKKLTLMLQ 220  
DB 383 VKLEEEKELTKELKLSLNKEKQLELQRAVLKMKIERIK 422

RESULT 35  
A47297  
myosin heavy chain form B, nonmuscle - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C>Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 02-Feb-2001  
C:Accession: A47297; A55441  
R:Bhatia-Dey, N.; Adelstein, R.S.; David, I.B.  
Proc. Natl. Acad. Sci. U.S.A. 90, 2856-2859, 1993  
A:Title: Cloning of the cDNA encoding a myosin heavy chain B isoform of Xenopus nonmu  
A:Reference number: A47297; MUID:93219383  
A:Accession: A47297  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-1992 <BHA>  
A:Cross-references: GB:L09740; NID:g214623; PIDN:AAA49915.1; PID:g214624  
A:Experimental source: XTC cells  
A>Note: sequence extracted from NCBI backbone (NCBI:P:128722)

R:Kelley, C.A.; Oberman, F.; Yisraeli, J.K.; Adelstein, R.S.  
 J. Biol. Chem. 270, 1395-1401, 1995  
 A:Title: A Xenopus nonmuscle myosin heavy chain isoform is phosphorylated by cyclin-p34  
 A:Reference number: A55441; MUID:95138137  
 A:Accession: A55441  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 198-232 <KEL>  
 C:Superfamily: myosin heavy chain; myosin motor domain homology  
 C:Keywords: nucleotide binding; P-loop  
 F:88-787/Domain: myosin motor domain homology <MOT>  
 F:178-185/Region: nucleotide-binding motif A (P-loop)

Query Match 14.1%; Score 150.5; DB 2; Length 1992;  
 Best Local Similarity 22.9%; Pred. No. 0.63;  
 Matches 58; Conservative 57; Mismatches 85; Indels 53; Gaps 9;

QY 4 INKLEFDLAQEEENV-----LDREF-----LKNELDNVRAQLSOK 38  
 Db 1093 IEELKQLAKKEEELQALARQDEEVLOKNNMTLKVLELQIAELQEDLESEKSRKA 1152  
 QY 39 DKERDSOVIITLDLTLEERNATVSIQALGKRAEMLCSTLKQKMYLEQOODETKQAQ 98  
 Db 1153 EKQRDLSEELALKTELEDTLDTTAAQOELTKRQEVAAELRKS-----EETRNHE 1206  
 QY 99 EEAGRLRSGKMT-MEQLLELLOSLPEVEEMIRDMGVGSAVE-----OLAVYCVSLRK-E 152  
 Db 1207 AQIQEMRQROATALE-----LSEQLQAKKRRVNI-EKKKOSLESNKELATEVKSLOQMK 1262  
 QY 153 YENIKKARKASGEV-----ADKLRRDLFSSRSKLTQTVYSELQAKLELSAQKDLQ 203  
 Db 1263 AESEKRRKLEGOVQELHAKVLEGRDLRADWKESSKIQ--NELENVSLLEAKKGI 1319  
 QY 204 SADKEINSLKKL 216  
 Db 1320 KLRDVASMESOL 1332

RESULT 36  
 JCS837  
 364K Golgi complex-associated protein - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 05-Mar-1998 #sequence:revision 13-Mar-1998 #text\_change 20-Jun-2000  
 C:Accession: JCS837  
 R:Toki, C.; Fujiwara, T.; Sohda, M.; Hong, H.S.; Msumi, Y.; Ikehara, Y.  
 Cell Struct. Funct. 22, 565-577, 1997  
 A:Title: Identification and characterization of rat 364-kDa Golgi-associated protein rec  
 A:Reference number: JCS837; MUID:98093490  
 A:Accession: JCS837  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-3187 <TOK>  
 A:Cross-references: DDBJ:D25543; NID:9516825; PIDN:BA05026.1; PID:9516826  
 C:Comment: This protein plays a role in the formation and maintenance of the characteris  
 C:Superfamily: giantin  
 F:49-549,624-1176,1238-1707,1763-3114/Domain: coiled-coil leucine zipper #status predict  
 F:3165-3187/Domain: membrane anchor #status predicted <MAD>

Query Match 14.1%; Score 150.5; DB 2; Length 3187;  
 Best Local Similarity 19.0%; Pred. No. 1;  
 Matches 58; Conservative 59; Mismatches 90; Indels 99; Gaps 7;

QY 10 DLADBEENVLDREFLKN---ELDNVRAQLSOKDKER-----DSQYIIDTLRDTLEER 59  
 Db 1310 ELESSQLADLEHLKTLQPLETLQKHVGNQKEEVSYLVQGLGEKQTLTTVQTEMEQ 1369  
 QY 60 NATVSL-----QALGKRAEMLCSTLKQKMYLEQOQ----- 91  
 Db 1370 ERLIKALHTQLEMOKKEERLKOVOYICELKQKOPKEEESNAKQOLQRLKALALISR 1429  
 QY 92 ----DETQAOEEAGRLRSKM-----KTMEQIELLQSLPEVEEMIRDMGVGSAVEOLA 143

Db 1430 KEALKENKSLQEQSSARDVAEHLTKSLADVESQVYQNGERDALGLKALLQGERDKLI 1489  
 QY 144 V-----YCVSLK----- 150  
 Db 1490 VEMDKSLLENQSLGSSCSLALQGLTDEKELKKELESVRCSTIAESTEOMKKEILO 1549  
 QY 151 KEVENLKARKASGEVAKRLKRDLPFSSRSKLTQTVYSELQAKLELSAQKDLQSDKREIM 210  
 Db 1550 KEVEFLQSYEVSNEARIRQHVVSVEQOEYAKLRSAESDKREKQLODAQOME 1609  
 QY 211 SLKKRL 216  
 Db 1610 EKKEK 1615

RESULT 37  
 S39082  
 myosin heavy chain, embryonic - chicken (fragment)  
 C:Species: Gallus gallus (chicken)  
 C:Date: 03-Feb-1994 #sequence:revision 03-Feb-1994 #text\_change 13-Aug-1999  
 C:Accession: S39082; S24349; A30170; S01265  
 R:Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.  
 submitted to the EMBL Data Library, August 1991  
 A:Description: Analysis of the chicken fast myosin heavy chain family: Localization o  
 A:Reference number: S39081  
 A:Accession: S39082  
 A:Molecule type: mRNA  
 A:Residues: 1-741 <MOO>  
 A:Cross-references: EMBL:M74086  
 A:Experimental source: clone Cem3  
 R:Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.  
 J. Mol. Biol. 225, 1143-1151, 1992  
 A:Title: Analysis of the chicken fast myosin heavy chain family. Localization of 1sof  
 A:Reference number: S24348; MUID:92309413  
 A:Accession: S24349  
 A:Molecule type: mRNA  
 A:Residues: 1-12,14-741 <MOO2>  
 A:Cross-references: EMBL:M74086  
 A:Experimental source: clone Cem3  
 R:Lagrutta, A.A.; McCarthy, J.G.; Scherzlinger, C.A.; Heywood, S.M.  
 DNA 8, 39-50, 1989  
 A:Title: Identification and developmental expression of a novel embryonic myosin hea  
 A:Reference number: A30170; MUID:89210285  
 A:Accession: A30170  
 A:Molecule type: DNA  
 A:Residues: 723-741 <LAG>  
 A:Cross-references: GB:M24691; NID:9341219; PIDN:AAA48950.1; PID:9531186  
 R:McCarthy, J.G.; Heywood, S.M.  
 Nucleic Acids Res. 15, 8069-8085, 1987  
 A:Title: A long polypyrimidine/polyurine tract induces an altered DNA conformation o  
 A:Reference number: S01265; MUID:88040428  
 A:Accession: S01265  
 A:Molecule type: DNA  
 A:Residues: 723-741 <MCC>  
 A:Cross-references: EMBL:X06251; NID:963600; PIDN:CAA29593.1; PID:963601  
 C:Superfamily: myosin heavy chain; myosin motor domain homology  
 C:Keywords: actin binding; ATP; coiled coil; muscle

Query Match 14.1%; Score 150; DB 2; Length 741;  
 Best Local Similarity 24.6%; Pred. No. 0.24;  
 Matches 61; Conservative 46; Mismatches 81; Indels 60; Gaps 10;

QY 10 DLADBEENVLDREFLKNELDNVRAQLSOKDKERDSOVIITLRLTLEERNATVYSLQQA 69  
 Db 3 DLSRELEI-----SEHLQVQKQL--EKEKSLKMEIDLDLSNME-----SVSKA 46  
 QY 70 LGRKEMLCSTLKQKMYLEQOODE-----TKQA--QEEAGRL----- 104  
 Db 47 KANLEKMRITLEDQSLKTKTEEEHQRMINDLNQRARLQTEAGEYSQVEEKDALISQL 106  
 QY 105 -RSKMTWEQIELLQSLPEVEEMIRDMGVGSAVEQLAVYCVSLKKEVENLKEAR--- 160

```
Db 107 SRGQAFVTOQEEELK-----HLEEEIKAKNALAHALQASRHDCLLREQYEEEOEAGCEL 162
Qy 161 -----KASGEVAD---KLRDLPFSRSKLTQVYSELDOAKLEKLSAKQDQSNKELMSL 212
Db 163 QRALSKANSEYAWKRYETDIAIQTLEELPAKKILAO---RLQDAEEHVEAVNAKASL 219
Qy 213 KKKLTMQ 220
Db 220 EKTQRIQ 227

RESULT 38
S02771
myosin heavy chain A [similarity] - Caenorhabditis elegans
N:Contents: myosin ATPase (EC 3.6.1.32)
C:Species: Caenorhabditis elegans
C>Date: 31-Dec-1993 #sequence_revision 19-May-2000 #text_change 19-Jan-2001
C:Accession: T23622; S02771
R:Harris, B.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z19773
A:Accession: T23622
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1992 <WIL>
A:Cross-references: EMBL:Z78199; PIDN:CA801576.1; GSPDB:GN00023; CESP:K12F2.1
A:Experimental source: Clone K12F2
R:Dbj, N.J.; Maruyama, I.N.; Krause, M.; Karn, J.
J. Mol. Biol. 205, 603-613, 1989
A:Title: Sequence analysis of the complete Caenorhabditis elegans myosin heavy chain gene
A:Reference number: S02771; MUID:89178677
A:Accession: S02771
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-116,140-1992 <DIB>
A:Cross-references: EMBL:X08067; NID:96798; PIDN:CAA30856.1; PID:96799
C:Genetics:
A:Gene: myo-3; CESP:K12F2.1
A:Map position: 5
A:Insertions: 46/1; 192/1; 292/1; 468/2; 1921/3
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; coiled coil; hydrolyase; methylated amino acid; muscle cd
F:89-802/Domain: myosin motor domain homology <MOT>
F:202-209/Region: nucleotide-binding motif A (P-loop)
F:690-712/Region: actin binding #status predicted
F:793-807/Region: actin binding #status predicted
F:875-1992/Domain: coiled coil #status predicted <COI>
F:875-1189/Region: S2
F:1190-1992/Region: light meromyosin
F:153/Modified site: N6,N6-trimethyllysine (lys) #status predicted
F:208/binding site: ATP (lys) #status predicted
F:730,740/Active site: Cys #status predicted

Query Match 14.1%; Score 150; DB 1; Length 1992;
Best Local Similarity 23.5%; Pred. No. 0.67;
Matches 64; Conservative 46; Mismatches 94; Indels 66; Gaps 10;
```

```
Db 1095 LKVAQENIDEITKQHDVETTLRKREEDLHHTNAKLAENNSIATLQRLIKELTARNAL 1154
Qy 189 -DOAKLEKSAOKDLOS---ADKEIMSLKKKL 216
Db 1155 EEELEAERNRSOKSDRSRPAERLEELTERL 1186

RESULT 39
S43554
plasmidogen-binding protein MUG72 - Streptococcus sp. (fragment)
C:Species: Streptococcus sp.
A:Variety: group G
C>Date: 07-Sep-1994 #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000
C:Accession: S45599; S43554
R:ben Nasr, A.; Wistedt, A.; Ringdahl, U.; Sjoebirg, U.
Eur. J. Biochem. 222, 267-276, 1994
A:Title: Streptokinase activates plasmidogen bound to human group C and G streptococci
A:Reference number: S45598; MUID:94291620
A:Accession: S45599
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-472 <BE2>
A:Cross-references: EMBL:Z32678; NID:9474769; PIDN:CAA83589.1; PID:91333838
C:Superfamily: M5 protein

Query Match 14.0%; Score 149; DB 2; Length 472;
Best Local Similarity 24.7%; Pred. No. 0.17;
Matches 59; Conservative 46; Mismatches 94; Indels 40; Gaps 7;

Qy 10 DLAGE-EENVLDREFLK-----NELDNVAQOLS-----QKDKRDSQVIL 49
Db 118 DLNDLEEKLDKREFYIGETLRTINEIDLKIGLNDINIDLKHELEKQKAEADROT-L 176
Qy 50 DTLRDLERNATVVSLOALGKAEMLCSTLKQMKYLEQDQDETKQAGEAG-IRSKM 108
Db 177 EAERKALEEEKQISDASRQSLRDLDSREAKQOLEAEYQKLEBEKQISDASRQSLRDL 236
Qy 109 KTMQIEILLQSLPEVE-----MIRMGVGSAGEVLAVYCSIKREYENLK 157
Db 237 DASREARKQLEAEYQKLEBEKQISEASRKGRLRDLDSREAKQO-----LEAEHOKLE 289
Qy 158 EARRKAGEVADLKRDKFFSSRSKLTQVYSELDQKLEKLSAKQDQSNKELMSLKKL 216
Db 290 EQNKISASRKGRLRDLDSREAKQYKQVEXDLANTAFELDKVKEKQISDPSRKGLRDL 348

RESULT 40
B72765
hypothetical protein APE0110 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 02-Feb-2001
C:Accession: B72765
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero
A:Reference number: A72450; MUID:99310339
A:Accession: B72765
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-919 <KAW>
A:Cross-references: DDBJ:A000058; NID:95103388; PIDN:BA79020.1; PID:95103499
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE0110
C:Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032

Query Match 14.0%; Score 149; DB 2; Length 919;
Best Local Similarity 23.1%; Pred. No. 0.34;
Matches 61; Conservative 52; Mismatches 83; Indels 68; Gaps 9;
```



```

QY 12 AQEEENVLDR-EFLKNELDNVRAQLSOK----DKEKRDQOYIIDTLRDTLEERNATVYSL 66
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 410 SEKPESVLERLDVAVINDLESKARALDQEPASALEAEARLVOALSMLEESGSAFCPCVCGA 469
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 67 QOALGKAEMLCSTLKKOMKYL----EQOODETKQAQEEAGRLRSKMKMTMEQIELLLQSOL 122
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 470 ELPPGRALAIARHRYRHEERLRLKAAKEKAAEAESRLQDKRR--RIELL-SRL 525
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 123 PEVEEMIRDMGVQOSAVQOLAVYCVSLKKEYENLKEARKASGEVADKLR----- 171
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 526 NQLEBGLRELGF--QTPEDLAKAEQKLMRLERLELKLKLENSLEKVRNLSREVALRE 583
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 172 -----KDLFSSRSKLQ-----TWYSELQAK 192
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 584 AKTRALEVILORLIGIKEEPAREKLTLSSESSEKLEERMLVSKAEDLATRLGITAYRSLDDL- 642
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 193 LELKSQOKDLOSADKEIMSLKKL 216
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 643 --LEKAREALEGVDEKLSAIERRL 664
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: September 4, 2002, 16:13:00  
 Job time: 3244 sec